```
*************************************************************
Reviewer Comments:
<210>   8
<211>   57
<212>   PRT
<213>   rbcS3C


<400>   8

Met Ala Ser Ser Val Met Ser Ser Ala Ala Val Ala Thr Arg Gly Asn
1                   5                   10                  15


Gly Ala Gln Ala Ser Met Val Ala Pro Phe Thr Gly Leu Lys Ser Thr
              20                  25                  30


Ala Ser Phe Pro Val Ser Arg Lys Gln Asn Leu Asp Ile Thr Ser Ile
         35                  40                  45


Ala Ser Asn Gly Gly Arg Val Ser Cys
   50                  55
```

Regarding the above "<213>" response: it is invalid, per 1.823 of the
Sequence Rules. The only valid "<213>" responses are: the Genus
species of the organism, "Artificial Sequence", or "Unknown".
"Artificial Sequence" and "Unknown" require explanation in the "<220>-
<223>" section: please clearly indicate the source of the genetic
material. Same error in Sequences 9-10.
****

Application No: 10581861   Version No: 1.0

Input Set:

Output Set:

Started: 2011-03-31 11:37:17.586

Finished: 2011-03-31 11:37:18.146

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 560 ms

Total Warnings: 7

Total Errors: 0

No. of SeqIDs Defined: 10

Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)

<210>   1
<211>   23
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   PRIMER

<400>   1
gcttgcaagg ggtaaccatg acg   23

<210>   2
<211>   21
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   PRIMER

<400>   2
tctagaggat caggcgatcg c   21

<210>   3
<211>   23
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   PRIMER

<400>   3

```
gcttgcaagg ggtaaccatg acg                                          23


<210>   4
<211>   21
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   PRIMER

<400>   4
tctagatccg ggtcactcga g                                            21


<210>   5
<211>   171
<212>   DNA
<213>   Lycopersicon esculentum

<400>   5
atggcttctt cagtaatgtc ctcagcagct gttgccaccc gcggcaatgg tgcacaagct    60

agcatggttg caccccttcac tggactcaag tccaccgctt ctttccctgt ttcaaggaag   120

caaaaccttg acattacctc cattgctagc aacggtggaa gagtcagttg c            171


<210>   6
<211>   633
<212>   DNA
<213>   Mycobacterium gastri

<400>   6
atgaagctcc aagtcgccat cgacctgctg tccaccgaag ccgccctcga gctggccggc    60

aaggttgccg agtacgtcga catcatcgaa ctgggcaccc ccctgatcga ggccgagggc   120

ctgtcggtca tcaccgccgt caagaaggct cacccggaca agatcgtctt cgccgacatg   180

aagaccatgg acgccggcga gctcgaagcc gacatcgcgt tcaaggccgg cgctgacctg   240

gtcacggtcc tcggctcggc cgacgactcc accatcgcgg gtgccgtcaa ggccgcccag   300

gctcacaaca agggcgtcgt cgtcgacctg atcggcatcg aggacaaggc cacccgtgca   360

caggaagttc gcgccctggg tgccaagttc gtcgagatgc acgctggtct ggacgagcag   420

gccaagcccg gcttcgacct gaacggtctg ctcgccgccg gcgagaaggc tcgcgttccg   480

ttctccgtgg ccggtggcgt gaaagttgcg accatccccg cagtccagaa ggccggcgca   540

gaagttgccg tcgccggtgg cgccatctac ggtgcagccg acccggccgc cgccgcgaag   600

gaactgcgcg ccgcgatcgc ctgatcctga tcg                               633
```

<210> 7
<211> 633
<212> DNA
<213> Mycobacterium gastri

<400> 7
atgaagctcc aagtcgccat cgacctgctg tccaccgaag ccgccctcga gctggccggc   60

aaggttgccg agtacgtcga catcatcgaa ctgggcaccc ccctgatcga ggccgagggc   120

ctgtcggtca tcaccgccgt caagaaggct cacccggaca agatcgtctt cgccgacatg   180

aagaccatgg acgccggcga gctcgaagcc gacatcgcgt tcaaggccgg cgctgacctg   240

gtcacggtcc tcggctcggc cgacgactcc accatcgcgg gtgccgtcaa ggccgcccag   300

gctcacaaca agggcgtcgt cgtcgacctg atcggcatcg aggacaaggc cacccgtgca   360

caggaagttc gcgccctggg tgccaagttc gtcgagatgc acgctggtct ggacgagcag   420

gccaagcccg gcttcgacct gaacggtctg ctcgccgccg gcgagaaggc tcgcgttccg   480

ttctccgtgg ccggtggcgt gaaagttgcg accatccccg cagtccagaa ggccggcgca   540

gaagttgccg tcgccggtgg cgccatctac ggtgcagccg acccggccgc cgccgcgaag   600

gaactgcgcg ccgcgatcgc ctgatcctga tcg   633

<210> 8
<211> 57
<212> PRT
<213> rbcS3C

<400> 8

Met Ala Ser Ser Val Met Ser Ser Ala Ala Val Ala Thr Arg Gly Asn
1   5   10   15

Gly Ala Gln Ala Ser Met Val Ala Pro Phe Thr Gly Leu Lys Ser Thr
            20   25   30

Ala Ser Phe Pro Val Ser Arg Lys Gln Asn Leu Asp Ile Thr Ser Ile
        35   40   45

Ala Ser Asn Gly Gly Arg Val Ser Cys
    50   55

<210> 9
<211> 207
<212> PRT
<213> rmpA

<400> 9

Met Lys Leu Gln Val Ala Ile Asp Leu Leu Ser Thr Glu Ala Ala Leu
1   5   10   15

Glu Leu Ala Gly Lys Val Ala Glu Tyr Val Asp Ile Ile Glu Leu Gly
                20   25   30

Thr Pro Leu Ile Glu Ala Glu Gly Leu Ser Val Ile Thr Ala Val Lys
        35   40   45

Lys Ala His Pro Asp Lys Ile Val Phe Ala Asp Met Lys Thr Met Asp
    50   55   60

Ala Gly Glu Leu Glu Ala Asp Ile Ala Phe Lys Ala Gly Ala Asp Leu
65   70   75   80

Val Thr Val Leu Gly Ser Ala Asp Asp Ser Thr Ile Ala Gly Ala Val
                85   90   95

Lys Ala Ala Gln Ala His Asn Lys Gly Val Val Val Asp Leu Ile Gly
                100   105   110

Ile Glu Asp Lys Ala Thr Arg Ala Gln Glu Val Arg Ala Leu Gly Ala
        115   120   125

Lys Phe Val Glu Met His Ala Gly Leu Asp Glu Gln Ala Lys Pro Gly
    130   135   140

Phe Asp Leu Asn Gly Leu Leu Ala Ala Gly Glu Lys Ala Arg Val Pro
145   150   155   160

Phe Ser Val Ala Gly Gly Val Lys Val Ala Thr Ile Pro Ala Val Gln
                165   170   175

Lys Ala Gly Ala Glu Val Ala Val Ala Gly Gly Ala Ile Tyr Gly Ala
                180   185   190

Ala Asp Pro Ala Ala Ala Ala Lys Glu Leu Arg Ala Ala Ile Ala
        195   200   205

<210>   10
<211>   199
<212>   PRT

<213> rmpB

<400> 10

Met Thr Gln Ala Ala Glu Ala Asp Gly Ala Val Lys Val Val Gly Asp
1   5   10   15

Asp Ile Thr Asn Asn Leu Ser Leu Val Arg Asp Glu Val Ala Asp Thr
            20   25   30

Ala Ala Lys Val Asp Pro Glu Gln Val Ala Val Leu Ala Arg Gln Ile
        35   40   45

Val Gln Pro Gly Arg Val Phe Val Ala Gly Ala Gly Arg Ser Gly Leu
    50   55   60

Val Leu Arg Met Ala Ala Met Arg Leu Met His Phe Gly Leu Thr Val
65   70   75   80

His Val Ala Gly Asp Thr Thr Thr Pro Ala Ile Ser Ala Gly Asp Leu
            85   90   95

Leu Leu Val Ala Ser Gly Ser Gly Thr Thr Ser Gly Val Val Lys Ser
            100   105   110

Ala Glu Thr Ala Lys Lys Ala Gly Ala Arg Ile Ala Ala Phe Thr Thr
            115   120   125

Asn Pro Asp Ser Pro Leu Ala Gly Leu Ala Asp Ala Val Val Ile Ile
    130   135   140

Pro Ala Ala Gln Lys Thr Asp His Gly Ser His Ile Ser Arg Gln Tyr
145   150   155   160

Ala Gly Ser Leu Phe Glu Gln Val Leu Phe Val Val Thr Glu Ala Val
            165   170   175

Phe Gln Ser Leu Trp Asp His Thr Glu Val Glu Ala Glu Glu Leu Trp
            180   185   190

Thr Arg His Ala Asn Leu Glu
        195